

FIG.1A

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                                1
ACTGCAACCCTAATCAGAGCCCAA    met ala gln trp glt met leu gln
                                ATG GCG CAG TGG GAA ATG CTG CAG

    10                                20
asn leu asp ser pro phe gln asp gln leu his gln leu tyr ser
AAT CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG

                                30
his ser leu leu pro val asp ile arg gln tyr leu ala val trp
CAC AGC CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG

    40                                50
ile glu asp gln asn trp gln glu ala ala leu gly ser asp asp
ATT GAA GAC CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT

                                60
ser lys ala thr met leu phe phe his phe leu asp gln leu asn.
TCC AAG GCT ACC ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC

    70                                80
tyr glu cys gly arg cys ser gln asp pro glu ser leu leu leu
TAT GAG TGT GGC CGT TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG

                                90
gln his asn leu arg lys phe cys arg asp ile gln pro phe ser
CAG CAC AAT TTG CGG AAA TTC TGC CGG GAC ATT CAG CCC TTT TCC

    100                                110
gln asp pro thr gln leu ala glu met ile phe asn leu leu leu
CAG GAT CCT ACC CAG TTG GCT GAG ATG ATC TTT AAC CTC CTT CTG

                                120
glu glu lys arg ile leu ile gln ala gln arg ala gln leu glu
GAA GAA AAA AGA ATT TTG ATC CAG GCT CAG AGG GCC CAA TTG GAA

    130                                140
gln gly glu pro val leu glu thr pro val glu ser gln gln his
CAA GGA GAG CCA GTT CTC GAA ACA CCT GTG GAG AGC CAG CAA CAT

                                150
glu ile glu ser arg ile leu asp leu arg ala met met glu lys
GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG GCT ATG ATG GAG AAG

    160                                170
leu val lys ser ile ser gln leu lys asp gln gln asp val phe
CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG CAG GAT GTC TTC

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FIG.1B

cys phe arg tyr lys ile gln ala lys gly lys thr pro ser leu
TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA CCC TCT CTG

190 200
asp pro his gln thr lys glu gln lys ile leu gln glu thr leu
GAC CCC CAT CAG ACC AAA GAG CAG AAG ATT CTG CAG GAA ACT CTC

210
asn glu leu asp lys arg arg lys glu val leu asp ala ser lys
AAT GAA CTG GAC AAA AGG AGA AAG GAG GTG CTG GAT GCC TCC AAA

220 230
ala leu leu gly arg leu thr thr leu ile glu leu leu leu pro
GCA CTG CTA GGC CGA TTA ACT ACC CTA ATC GAG CTA CTG CTG CCA

240
lys leu glu glu trp lys ala gln gln gln lys ala cys ile arg
AAG TTG GAG GAG TGG AAG GCC CAG CAG CAA AAA GCC TGC ATC AGA

250 260
ala pro ile asp his gly leu glu gln leu glu thr trp phe thr
GCT CCC ATT GAC CAC GGG TTG GAA CAG CTG GAG ACA TGG TTC ACA

270
ala gly ala lys leu leu phe his leu arg gln leu leu lys glu
GCT GGA GCA AAG CTG TTG TTT CAC CTG AGG CAG CTG CTG AAG GAG

280 290
leu lys gly leu ser cys leu val ser tyr gln asp asp pro leu
CTG AAG GGA CTG AGT TGC CTG GTT AGC TAT CAG GAT GAC CCT CTG

300
thr lys gly val asp leu arg asn ala gln val thr glu leu leu
ACC AAA GGG GTG GAC CTA CGC AAC GCC CAG GTC ACA GAG TTG CTA

310 320
gln arg leu leu his arg ala phe val val glu thr gln pro cys
CAG CGT CTG CTC CAC AGA GCC TTT GTG GTA GAA ACC CAG CCC TGC

330
met pro gln thr pro his arg pro leu ile leu lys thr gly ser
ATG CCC CAA ACT CCC CAT CGA CCC CTC ATC CTC AAG ACT GGC AGC

340 350
lys phe thr val arg thr arg leu leu val arg leu gln glu gly
AAG TTC ACC GTC CGA ACA AGG CTG CTG GTG AGA CTC CAG GAA GGC

360
asn glu ser leu thr val glu val ser ile asp arg asn pro pro
AAT GAG TCA CTG ACT GTG GAA GTC TCC ATT GAC AGG AAT CCT CCT

370 380
gln leu gln gly phe arg lys phe asn ile leu thr ser asn gln
CAA TTA CAA GGC TTC CGG AAG TTC AAC ATT CTG ACT TCA AAC CAG

390
lys thr leu thr pro glu lys gly gln ser gln gly leu ile trp

FIG.1C

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AAA ACT TTG ACC CCC GAG AAG GGG CAG AGT CAG GGT TTG ATT TGG

      400                                     410
asp phe gly tyr leu thr leu val glu gln arg ser gly gly ser
GAC TTT GGT TAC CTG ACT CTG GTG GAG CAA CGT TCA GGT GGT TCA

                                420
gly lys gly ser asn lys gly pro leu gly val thr glu glu leu
GGA AAG GGC AGC AAT AAG GGG CCA CTA GGT GTG ACA GAG GAA CTG

      430                                     440
his ile ile ser phe thr val lys tyr thr tyr gln gly leu lys
CAC ATC ATC AGC TTC ACG GTC AAA TAT ACC TAC CAG GGT CTG AAG

                                450
gln glu leu lys thr asp thr leu pro val val ile ile ser asn
CAG GAG CTG AAA ACG GAC ACC CTC CCT GTG GTG ATT ATT TCC AAC

      460                                     470
met asn gln leu ser ile ala trp ala ser val leu trp phe asn
ATG AAC CAG CTC TCA ATT GCC TGG GCT TCA GTT CTC TGG TTC AAT

                                480
leu leu ser pro asn leu gln asn gln gln phe phe ser asn pro
TTG CTC AGC CCA AAC CTT CAG AAC CAG CAG TTC TTC TCC AAC CCC

      490                                     500
pro lys ala pro trp ser leu leu gly pro ala leu ser trp gln
CCC AAG GCC CCC TGG AGC TTG CTG GGC CCT GCT CTC AGT TGG CAG

                                510
phe ser ser tyr val gly arg gly leu asn ser asp gln leu ser
TTC TCC TCC TAT GTT GGC CGA GGC CTC AAC TCA GAC CAG CTG AGC

      520                                     530
met leu arg asn lys leu phe gly gln asn cys arg thr glu asp
ATG CTG AGA AAC AAG CTG TTC GGG CAG AAC TGT AGG ACT GAG GAT

                                540
pro leu leu ser trp ala asp phe thr lys arg glu ser pro pro
CCA TTA TTG TCC TGG GCT GAC TTC ACT AAG CGA GAG AGC CCT CCT

      550                                     560
gly lys leu pro phe trp thr trp leu asp lys ile leu glu leu
GGC AAG TTA CCA TTC TGG ACA TGG CTG GAC AAA ATT CTG GAG TTG

                                570
val his asp his leu lys asp leu trp asn asp gly arg ile met
GTA CAT GAC CAC CTG AAG GAT CTC TGG AAT GAT GGA CGC ATC ATG

      580                                     590
gly phe val ser arg ser gln glu arg arg leu leu lys lys thr
GGC TTT GTG AGT CGG AGC CAG GAG CGC CGG CTG CTG AAG AAG ACC

                                600
met ser gly thr phe leu leu arg phe ser glu ser ser glu gly
ATG TCT GGC ACC TTT CTA CTG CGC TTC AGT GAA TCG TCA GAA GGG

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FIG.1D

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      610                                620
gly ile thr cys ser trp val glu his gln asp asp asp lys val
GGC ATT ACC TGC TCC TGG GTG GAG CAC CAG GAT GAT GAC AAG GTG

      630
leu ile tyr ser val gln pro tyr thr lys glu val leu gln ser
CTC ATC TAC TCT GTG CAA CCG TAC ACG AAG GAG GTG CTG CAG TCA

      640                                650
leu pro leu thr glu ile ile arg his tyr gln leu leu thr glu
CTC CCG CTG ACT GAA ATC ATC CGC CAT TAC CAG TTG CTC ACT GAG

      660
glu asn ile pro glu asn pro leu arg phe leu tyr pro arg ile
GAG AAT ATA CCT GAA AAC CCA CTG CGC TTC CTC TAT CCC CGA ATC

      670                                680
pro arg asp glu ala phe gly cys tyr tyr gln glu lys val asn
CCC CGG GAT GAA GCT TTT GGG TGC TAC TAC CAG GAG AAA GTT AAT

      690
leu gln glu arg arg lys tyr leu lys his arg leu ile val val
CTC CAG GAA CGG AGG AAA TAC CTG AAA CAC AGG CTC ATT GTG GTC

      700                                710
ser asn arg gln val asp glu leu gln gln pro leu glu leu lys
TCT AAT AGA CAG GTG GAT GAA CTG CAA CAA CCG CTG GAG CTT AAG

      720
pro glu pro glu leu glu ser leu glu leu glu leu gly leu val
CCA GAG CCA GAG CTG GAG TCA TTA GAG CTG GAA CTA GGG CTG GTG

      730                                740
pro glu pro glu leu ser leu asp leu glu pro leu leu lys ala
CCA GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA

      750
gly leu asp leu gly pro glu leu glu ser val leu glu ser thr
GGG CTG GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT

      760                                770
leu glu pro val ile glu pro thr leu cys met val ser gln thr
CTG GAG CCT GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA

      780
val pro glu pro asp gln gly pro val ser gln pro val pro glu
GTG CCA GAG CCA GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG

      790                                800
pro asp leu pro cys asp leu arg his leu asn thr glu pro met
CCA GAT TTG CCC TGT GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG

      810
glu ile phe arg asn cys val lys ile glu glu ile met pro asn
GAA ATC TTC AGA AAC TGT GTA AAG ATT GAA GAA ATC ATG CCG AAT
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FIG.1E

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      820                                830
gly asp pro leu leu ala gly gln asn thr val asp glu val tyr
GGT GAC CCA CTG TTG GCT GGC CAG AAC ACC GTG GAT GAG GTT TAC

                                840
val ser arg pro ser his phe tyr thr asp gly pro leu met pro
GTC TCC CGC CCC AGC CAC TTC TAC ACT GAT GGA CCC TTG ATG CCT

      850 851
ser asp phe AM
TCT GAC TTC TAG GAACCACATTTCTCTGTTCTTTTCATATCTCTTTGCCCTTCCTA
CTCCTCATAGCATGATATTGTTCTCCAAGGATGGGAATCAGGCATGTGTCCCTTCCAAGC
TGTGTTAACTGTTCAAACCTCAGGCCTGTGTGACTCCATTGGGGTGAGAGGTGAAAGCATA
ACATGGGTACAGAGGGGACAACAATGAATCAGAACAGATGCTGAGCCATAGGTCTAAATA
GGATCCTGGAGGCTGCCTGCTGTGCTGGGAGGTATAGGGGTCCTGGGGGCAGGCCAGGGC
AGTTGACAGGTACTTGGAGGGCTCAGGGCAGTGGCTTCTTTCCAGTATGGAAGGATTTCA
ACATTTTAATAGTTGGTTAGGCTAAACTGGTGCATACTGGCATTGGCCTTGGTGGGGAGC
ACAGACACAGGATAGGACTCCATTTCTTTCTTCCATTCCCTTCATGTCTAGGATAACTTGC
TTTCTTCTTTTCCTTTTACTCCTGGCTCAAGCCCTGAATTTCTTCTTTTCCTGCAAGGGGTTG
AGAGCTTTCTGCCTTAGCCTACCATGTGAAACTCTACCCTGAAGAAAGGGATGGATAGGA
AGTAGACCTCTTTTTCTTACCAGTCTCCTCCCCTACTCTGCCCCCTAAGCTGGCTGTACC
TGTTCTCCCCCATAAAATGATCCTGCCAATCTAAAAAAAAA
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FIG. 2A

ATTAAACCTCTCGCCGAGCCCTCCGCAGACTCTGCGCCGGAAAGTTTCATTTGCTGTATGCCA

TCCTCGAGAGCTGTCTAGGTTAACGTTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCACC

TAACGTGCTGTGCGTAGCTGCTCCTTTGGTTGAATCCCCAGGCCCTTGTGTTGGGGCACAAGGTGG

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu
CAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC TCA AAA TTC CTG

Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg
GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC ATG GAA ATC AGA

Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala
CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG GAG CAC GCT GCC

Asn	Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln
AAT	GAT	GTT	TCA	TTT	GCC	ACC	ATC	CGT	TTT	CAT	GAC	CTC	CTG	TCA	CAG

Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu
CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT AAC TTC TTG CTA

Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln
CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG GAT AAT TTT CAG

Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu
GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC TGT CTG AAG GAA

Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser
GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT CAG GCT CAG TCG

Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp
GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG AAA GAG CTT GAC

Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu
AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT ATA GAG CAT GAA

Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys
ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC TTC AAA TGC AAA

Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp
ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG GCA AAG AGT GAT

Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys M t Tyr Leu Met Leu Asp
CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT TTA ATG CTT GAC

Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val
AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG TTG CTG AAT GTC

FIG. 2B

Thr	Glu	Leu	Thr	Gln	Asn	Ala	Leu	Ile	Asn	Asp	Glu	Leu	Val	Glu	Trp
ACT	GAA	CTT	ACC	CAG	AAT	GCC	CTG	ATT	AAT	GAT	GAA	CTA	GTG	GAG	TGG
Lys	Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala	Cys
AAG	CGG	AGA	CAG	CAG	AGC	GCC	TGT	ATT	GGG	GGG	CCG	CCC	AAT	GCT	TGC
Leu	Asp	Gln	Leu	Gln	Asn	Trp	Phe	Thr	Ile	Val	Ala	Glu	Ser	Leu	Gln
TTG	GAT	CAG	CTG	CAG	AAC	TGG	TTC	ACT	ATA	GTT	GCG	GAG	AGT	CTG	CAG
Gln	Val	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Tyr
CAA	GTT	CGG	CAG	CAG	CTT	AAA	AAG	TTG	GAG	GAA	TTG	GAA	CAG	AAA	TAC
Thr	Tyr	Glu	His	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Trp	Asp
ACC	TAC	GAA	CAT	GAC	CCT	ATC	ACA	AAA	AAC	AAA	CAA	GTG	TTA	TGG	GAC
Arg	Thr	Phe	Ser	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val
CGC	ACC	TTC	AGT	CTT	TTC	CAG	CAG	CTC	ATT	CAG	AGC	TCG	TTT	GTG	GTG
Glu	Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu
GAA	AGA	CAG	CCC	TGC	ATG	CCA	ACG	CAC	CCT	CAG	AGG	CCG	CTG	GTC	TTG
Lys	Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Val	Lys	Leu
AAG	ACA	GGG	GTC	CAG	TTC	ACT	GTG	AAG	TTG	AGA	CTG	TTG	GTG	AAA	TTG
Gln	Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	Phe	Asp	Lys	Asp
CAA	GAG	CTG	AAT	TAT	AAT	TTG	AAA	GTC	AAA	GTC	TTA	TTT	GAT	AAA	GAT
Val	Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu
GTG	AAT	GAG	AGA	AAT	ACA	GTA	AAA	GGA	TTT	AGG	AAG	TTC	AAC	ATT	TTG
Gly	Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly	Ser
GGC	ACG	CAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	TCC	ACC	AAT	GGC	AGT
Leu	Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn	Ala
CTG	GCG	GCT	GAA	TTT	CGG	CAC	CTG	CAA	TTG	AAA	GAA	CAG	AAA	AAT	GCT
Gly	Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu	His
GGC	ACC	AGA	ACG	AAT	GAG	GGT	CCT	CTC	ATC	GTT	ACT	GAA	GAG	CTT	CAC
Ser	Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile	Asp
TCC	CTT	AGT	TTT	GAA	ACC	CAA	TTG	TGC	CAG	CCT	GGT	TTG	GTA	ATT	GAC
Leu	Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser	Gln
CTC	GAG	ACG	ACC	TCT	CTG	CCC	GTT	GTG	GTG	ATC	TCC	AAC	GTC	AGC	CAG
Leu	Pro	S r	Gly	Trp	Ala	S r	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Ala
CTC	CCG	AGC	GGT	TGG	GCC	TCC	ATC	CTT	TGG	TAC	AAC	ATG	CTG	GTG	GCG
Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	Cys	Ala	Arg	Trp
GAA	CCC	AGG	AAT	CTG	TCC	TTC	TTC	CTG	ACT	CCA	CCA	TGT	GCA	CGA	TGG

FIG. 2C

Ala	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys
GCT	CAG	CTT	TCA	GAA	GTG	CTG	AGT	TGG	CAG	TTT	TCT	TCT	GTC	ACC	AAA
Arg	Gly	Leu	Asn	Val	Asp	Gln	Leu	Asn	Met	Leu	Gly	Glu	Lys	Leu	Leu
AGA	GGT	CTC	AAT	GTG	GAC	CAG	CTG	AAC	ATG	TTG	GGA	GAG	AAG	CTT	CTT
Gly	Pro	Asn	Ala	Ser	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys
GGT	CCT	AAC	GCC	AGC	CCC	GAT	GGT	CTC	ATT	CCG	TGG	ACG	AGG	TTT	TGT
Lys	Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Pro	Phe	Trp	Leu	Trp	Ile	Glu
AAG	GAA	AAT	ATA	AAT	GAT	AAA	AAT	TTT	CCC	TTC	TGG	CTT	TGG	ATT	GAA
Ser	Ile	Leu	Glu	Leu	Ile	Lys	Lys	His	Leu	Leu	Pro	Leu	Trp	Asn	Asp
AGC	ATC	CTA	GAA	CTC	ATT	AAA	AAA	CAC	CTG	CTC	CCT	CTC	TGG	AAT	GAT
Gly	Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	Arg	Ala	Leu	Leu
GGG	TGC	ATC	ATG	GGC	TTC	ATC	AGC	AAG	GAG	CGA	GAG	CGT	GCC	CTG	TTG
Lys	Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser
AAG	GAC	CAG	CAG	CCG	GGG	ACC	TTC	CTG	CTG	CGG	TTC	AGT	GAG	AGC	TCC
Arg	Glu	Gly	Ala	Ile	Thr	Phe	Thr	Trp	Val	Glu	Arg	Ser	Gln	Asn	Gly
CGG	GAA	GGG	GCC	ATC	ACA	TTC	ACA	TGG	GTG	GAG	CGG	TCC	CAG	AAC	GGA
Gly	Glu	Pro	Asp	Phe	His	Ala	Val	Glu	Pro	Tyr	Thr	Lys	Lys	Glu	Leu
GGC	GAA	CCT	GAC	TTC	CAT	GCG	GTT	GAA	CCC	TAC	ACG	AAG	AAA	GAA	CTT
Ser	Ala	Val	Thr	Phe	Pro	Asp	Ile	Ile	Arg	Asn	Tyr	Lys	Val	Met	Ala
TCT	GCT	GTT	ACT	TTC	CCT	GAC	ATC	ATT	CGC	AAT	TAC	AAA	GTC	ATG	GCT
Ala	Glu	Asn	Ile	Pro	Glu	Asn	Pro	Leu	Lys	Tyr	Leu	Tyr	Pro	Asn	Ile
GCT	GAG	AAT	ATT	CCT	GAG	AAT	CCC	CTG	AAG	TAT	CTG	TAT	CCA	AAT	ATT
Asp	Lys	Asp	His	Ala	Phe	Gly	Lys	Tyr	Tyr	Ser	Arg	Pro	Lys	Glu	Ala
GAC	AAA	GAC	CAT	GCC	TTT	GGA	AAG	TAT	TAC	TCC	AGG	CCA	AAG	GAA	GCA
Pro	Glu	Pro	Met	Glu	Leu	Asp	Gly	Pro	Lys	Gly	Thr	Gly	Tyr	Ile	Lys
CCA	GAG	CCA	ATG	GAA	CTT	GAT	GGC	CCT	AAA	GGA	ACT	GGA	TAT	ATC	AAG
Thr	Glu	Leu	Ile	Ser	Val	Ser	Glu	Val	His	Pro	Ser	Arg	Leu	Gln	Thr
ACT	GAG	TTG	ATT	TCT	GTG	TCT	GAA	GTT	CAC	CCT	TCT	AGA	CTT	CAG	ACC
Thr	Asp	Asn	Leu	Leu	Pro	Met	Ser	Pro	Glu	Glu	Phe	Asp	Glu	Val	Ser
ACA	GAC	AAC	CTG	CTC	CCC	ATG	TCT	CCT	GAG	GAG	TTT	GAC	GAG	GTG	TCT
Arg	Ile	Val	Gly	Ser	Val	Glu	Phe	Asp	Ser	Met	Met	Asn	Thr	Val	
CGG	ATA	GTG	GGC	TCT	GTA	GAA	TTC	GAC	AGT	ATG	ATG	AAC	ACA	GTA	TAG

AGCATGAATTTTTTTCATCTTCTCTGGCGACAGTTTTTCCTTCTCATCTGTGATTCCCTCCTGCT

FIG. 2D

ACTCTGTTTCCTTCACATCCTGTGTTTCTAGGGAAATGAAAGAAAGGCCAGCAAATTCGCTGCA
ACCTGTTGATAGCAAGTGAATTTTTCTCTAACTCAGAAACATCAGTTACTCTGAAGGGCATCA
TGCATCTTACTGAAGGTAAAATTGAAAGGCATTCTCTGAAGAGTGGGTTTCACAAGTGAAAAA
CATCCAGATACACCCAAAGTATCAGGACGAGAATGAGGGTCCTTTGGGAAAGGAGAAGTTAAG
CAACATCTAGCAAATGTTATGCATAAAGTCAGTGCCCAACTGTTATAGGTTGTTGGATAAATC
AGTGGTTATTTAGGGAACTGCTTGACGTAGGAACGGTAAATTTCTGTGGGAGAATTCTTACAT
GTTTTCTTTGCTTTAAGTGTAAGTGGCAGTTTTCCATTGGTTTACCTGTGAAATAGTTCAAAG
CCAAGTTTATATACAATTATATCAGTCCTCTTTCAAAGGTAGCCATCATGGATCTGGTAGGGG
GAAATGTGTATTTTATTACATCTTTCACATTGGCTATTTAAAGACAAAGACAAATTCTGTTT
CTTGAGAAGAGAAATTTCCAAATTCACAAGTTGTGTTTGATATCCAAAGCTGAATACATTCTG
CTTTCATCTTGGTCACATACAATTATTTTTACAGTTCTCCCAAGGGAGTTAGGCTATTCACAA
CCACTCATTCAAAAGTTGAAATTAACCATAGATGTAGATAAACTCAGAAATTTAATTCATGTT
TCTTAAATGGGCTACTTTGTCTTTTTTGTATTAGGGTGGTATTTAGTCTATTAGCCACAAAA
TTGGGAAAGGAGTAGAAAAAGCAGTAACTGACAACTTGAATAATACACCAGAGATAATATGAG
AATCAGATCATTTCAAACCTCATTTCCATGTAACTGCATTGAGAACTGCATATGTTTCGCTG
ATATATGTGTTTTTCACATTTGCGAATGGTTCCATTCTCTCTCCTGTACTTTTTCCAGACACT
TTTTTGAGTGGATGATGTTTCGTGAAGTATACTGTATTTTTACCTTTTTTCCTTCCTTATCACT
GACACAAAAAGTAGATTAAGAGATGGGTTTGACAAGGTTCTTCCCTTTTACATACTGCTGTCT
ATGTGGCTGTATCTTGTTTTTCCACTACTGCTACCACAACCTATATTATCATGCAAATGCTGTA
TTCTTCTTTGGTGGAGATAAAGATTTCTTGAGTTTTGTTTTAAATTAAGCTAAAGTATCTG
TATTGCATTAAATATAATATCGACACAGTGCTTTCCGTGGCACTGCATACAATCTGAGGCCTC
CTCTCTCAGTTTTTTATATAGATGGCGAGAACCCTAAGTTTCAGTTGATTTTACAATTGAAATGA
CTAAAAAACAAAGAAGACAACATTAAAAACAATATTGTTTCTA

FIG. 3A

ATTAAACCTCTCGCCGAGCCCCCTCCGCAGACTCTGCGCCGGAAAGTTTCATTTGCTGTATGCC
ATCCTCGAGAGCTGTCTAGGTTAACGTTTCGCACTCTGTGTATATAACCTCGACAGTCTTGGCA
CCTAACGTGCTGTGCGTAGCTGCTCCTTTGGTTGAATCCCCAGGCCCTTGTTGGGGCACAAGG

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe
TGGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC TCA AAA TTC

Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile
CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC ATG GAA ATC

Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala
AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG GAG CAC GCT

Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser
GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC CTC CTG TCA

Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu
CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT AAC TTC TTG

Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe
CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG GAT AAT TTT

Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys
CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC TGT CTG AAG

Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln
GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT CAG GCT CAG

Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu
TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG AAA GAG CTT

Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His
GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT ATA GAG CAT

Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys
GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC TTC AAA TGC

Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser
AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG GCA AAG AGT

Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu
GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT TTA ATG CTT

Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn
GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG TTG CTG AAT

Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu
GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA CTA GTG GAG

FIG. 3B

Trp	Lys	Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala		
TGG	AAG	CGG	AGA	CAG	CAG	AGC	GCC	TGT	ATT	GGG	GGG	CCG	CCC	AAT	GCT		
Cys	Leu	Asp	Gln	Leu	Gln	Asn	Trp	Phe	Thr	Ile	Val	Ala	Glu	Ser	Leu		
TGC	TTG	GAT	CAG	CTG	CAG	AAC	TGG	TTC	ACT	ATA	GTT	GCG	GAG	AGT	CTG		
Gln	Gln	Val	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys		
CAG	CAA	GTT	CGG	CAG	CAG	CTT	AAA	AAG	TTG	GAG	GAA	TTG	GAA	CAG	AAA		
Tyr	Thr	Tyr	Glu	His	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Trp		
TAC	ACC	TAC	GAA	CAT	GAC	CCT	ATC	ACA	AAA	AAC	AAA	CAA	GTG	TTA	TGG		
Asp	Arg	Thr	Phe	Ser	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val		
GAC	CGC	ACC	TTC	AGT	CTT	TTC	CAG	CAG	CTC	ATT	CAG	AGC	TCG	TTT	GTG		
Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val		
GTG	GAA	AGA	CAG	CCC	TGC	ATG	CCA	ACG	CAC	CCT	CAG	AGG	CCG	CTG	GTC		
Leu	Lys	Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Leu	Arg	Leu	Leu	Val	Lys		
TTG	AAG	ACA	GGG	GTC	CAG	TTC	ACT	GTG	AAG	TTG	AGA	CTG	TTG	GTG	AAA		
Leu	Gln	Glu	Leu	Asn	Tyr	Asn	Leu	Lys	Val	Lys	Val	Leu	Phe	Asp	Lys		
TTG	CAA	GAG	CTG	AAT	TAT	AAT	TTG	AAA	GTC	AAA	GTC	TTA	TTT	GAT	AAA		
Asp	Val	Asn	Glu	Arg	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile		
GAT	GTG	AAT	GAG	AGA	AAT	ACA	GTA	AAA	GGA	TTT	AGG	AAG	TTC	AAC	ATT		
Leu	Gly	Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly		
TTG	GGC	ACG	CAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	TCC	ACC	AAT	GGC		
Ser	Leu	Ala	Ala	Glu	Phe	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn		
AGT	CTG	GCG	GCT	GAA	TTT	CGG	CAC	CTG	CAA	TTG	AAA	GAA	CAG	AAA	AAT		
Ala	Gly	Thr	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu		
GCT	GGC	ACC	AGA	ACG	AAT	GAG	GGT	CCT	CTC	ATC	GTT	ACT	GAA	GAG	CTT		
His	Ser	Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile		
CAC	TCC	CTT	AGT	TTT	GAA	ACC	CAA	TTG	TGC	CAG	CCT	GGT	TTG	GTA	ATT		
Asp	Leu	Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser		
GAC	CTC	GAG	ACG	ACC	TCT	CTG	CCC	GTT	GTG	GTG	ATC	TCC	AAC	GTC	AGC		
Gln	Leu	Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val		
CAG	CTC	CCG	AGC	GGT	TGG	GCC	TCC	ATC	CTT	TGG	TAC	AAC	ATG	CTG	GTG		
Ala	Glu	Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Thr	Pro	Pro	Cys	Ala	Arg		
GCG	GAA	CCC	AGG	AAT	CTG	TCC	TTC	TTC	CTG	ACT	CCA	CCA	TGT	GCA	CGA		
Trp	Ala	Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr		
TGG	GCT	CAG	CTT	TCA	GAA	GTG	CTG	AGT	TGG	CAG	TTT	TCT	TCT	GTC	ACC		

FIG. 3C

Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu
 AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA GAG AAG CTT

 Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe
 CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG ACG AGG TTT

 Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile
 TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG CTT TGG ATT

 Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn
 GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT CTC TGG AAT

 Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu
 GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG CGT GCC CTG

 Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser
 TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC AGT GAG AGC

 Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn
 TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG TCC CAG AAC

 Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu
 GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG AAG AAA GAA

 Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met
 CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC AAA GTC ATG

 Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn
 GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG TAT CCA AAT

 Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu
 ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG CCA AAG GAA

 Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile
 GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT GGA TAT ATC

 Lys Thr Glu Leu Ile Ser Val Ser Glu Val

 AAG ACT GAG TTG ATT TCT GTG TCT GAA GTG TAAGTGAACACAGAAGAGTGACA

 TGTTTACAAACCTCAAGCCAGCCTTGCTCCTGGCTGGGGCCTGTTGAAGATGCTTGTATTTTA

 CTTTTCCATTGTAATTGCTATCGCCATCACAGCTGAACTTGTTGAGATCCCCGTGTTACTGCC

 TATCAGCATTTTACTACTTTAAAAAAGCCAAAAACCAAATTTGTATTTAAGGT

 ATATAAATTTTCCCAAACCTGATACCCTTTGAAAAAGTATAAATAAAATGAGCAAAAGTTGAA

FIG. 4

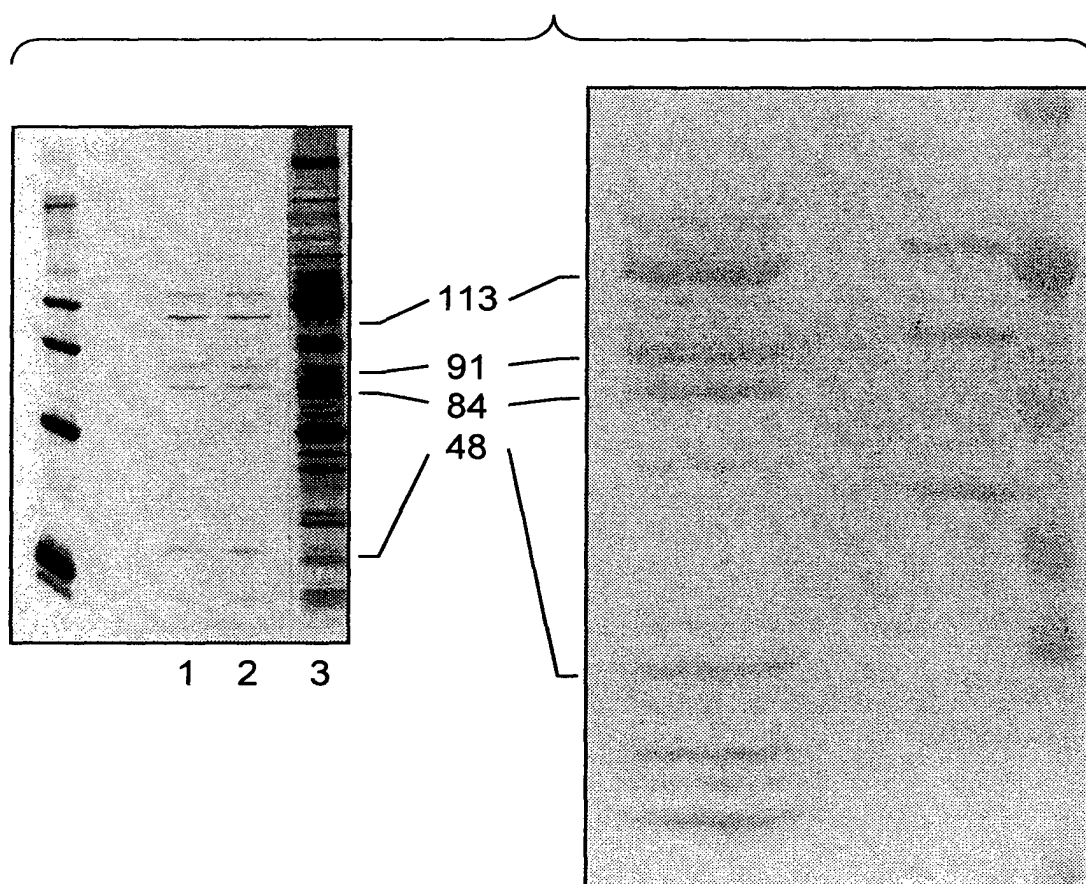


FIG. 5A

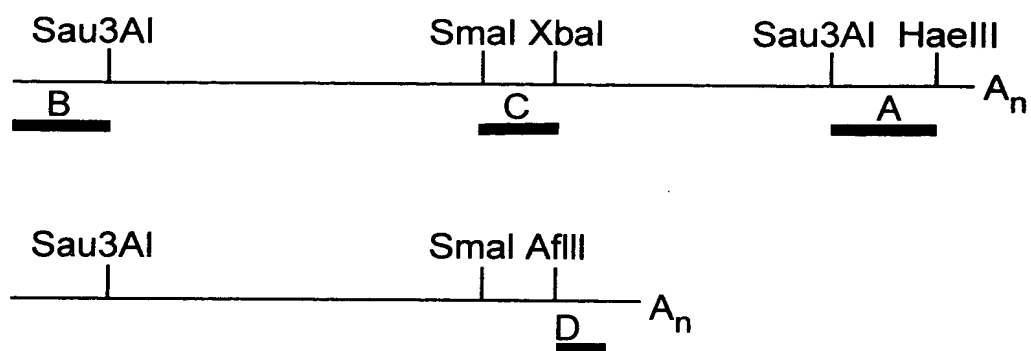


FIG. 5B

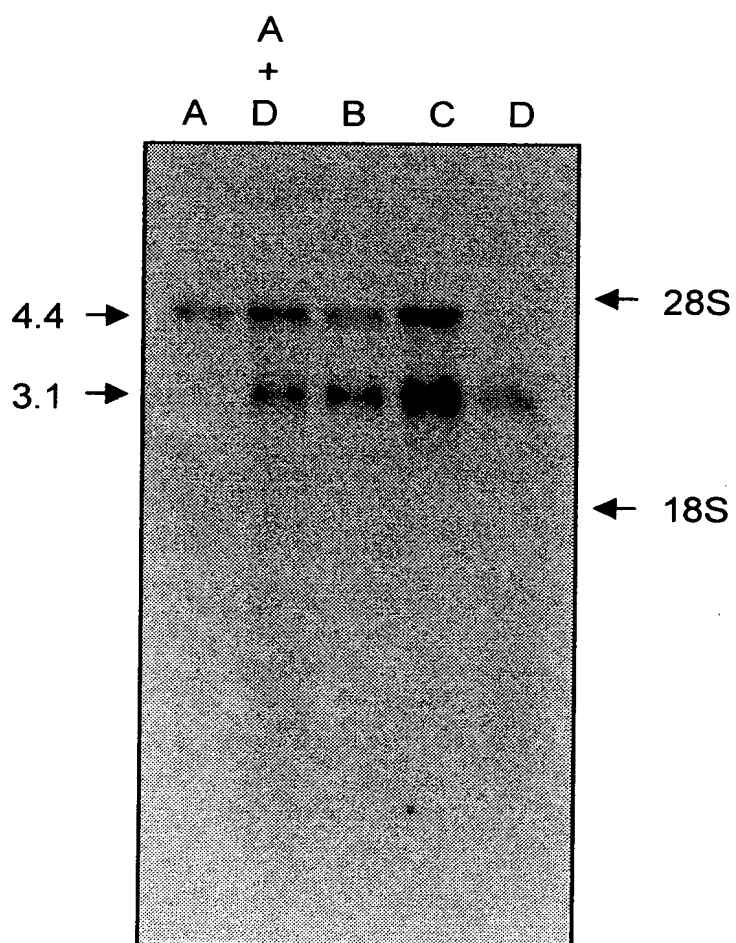


FIG. 6

1 MSQWYELQQLDSEKFLQVHQLYDDSFPMQIRQYLAQWLEKQDWEHAANDV
51 SFATIRFHDLLSQLDDQYSRFSLENNFLLQHNIRKSKRNLDQDNFQEDPIQ
101 MSMIIYSCLKEERKILENAQRFNQAQSGNIQSTVMLDKQKELDSKVRNVK
151 DKVMCIEHEIKSLEDLQDEYDFKCKTLQNHETNGVAKSDQKQEQLLLK
201 KMYLMLDNKRKEVVHKIIELLNVTELTQNALINDELVEWKRRQQSACIGG
251 PPNACLDQLQQVRQQLKKLEELEQKYTYEHPITKNKQVLWDRTFSLFQQ
301 LIQSSFVVERQPCMPHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVK
351 VLFDKDVNERNTVKGFRKFNILGTHEKVMNMEESTNGSLAAEFRLQLKE
401 QKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVISNV
451 SQLPSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLQSWQFSSVTK
127
501 RGLNVDOLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESI
119
551 LELIKHLLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGA
601 ITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPE
113a
651 NPLKYLYPNIDKDHAFGKYYSRPKEAPEPEMELDGPKGTGYIKTELISVSE
113b
701 VHPSRLQTTDNLLPMSPEEPDEVSRIVGSVEFDSMMNTV
↑
last amino acid of 84 kd

FIG. 7A

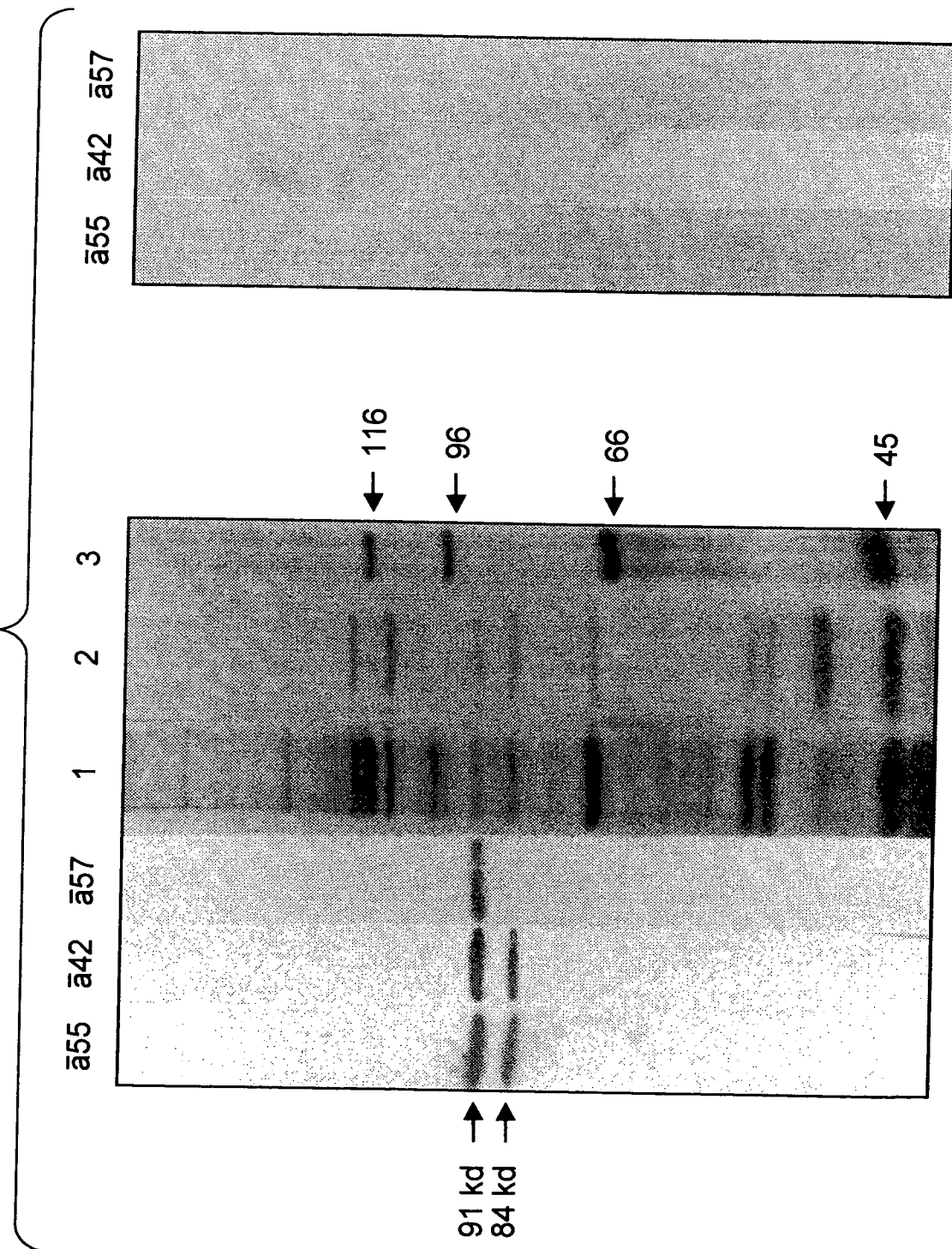


FIG. 7B

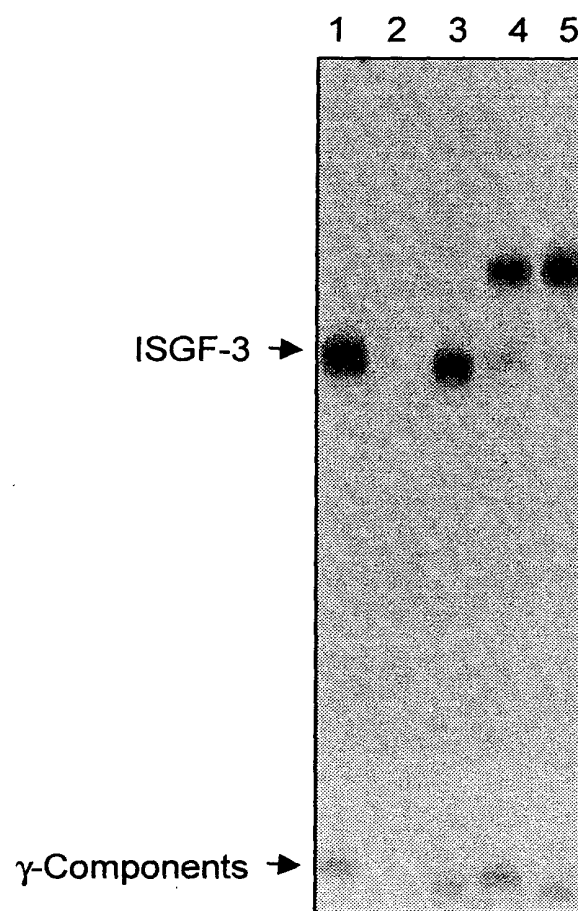


FIG. 8a

1: MAQWEMLNLDSPFQDQLHQLYSHSLPVDIRQYLAVWIEDQNWQEAALGSDDDSKATMLF

61: FHFDQLNYECGRCSQDPESLLQHNLNRKFCRDIQPFSDPTQLAEMIFNLLLEEKRII

121: QAQRAQLEQGEPVLETPVESQQHEIESRIDLDRAMMEKLVKSISQLKDQQDVFCERYKIQ

181: AKGKTPSLDPHQTKAQILQETLNELDKRRKEVLDASKALLGRLTTLIELLLPKLEEWKA

241: QQQKACIRAPIDHGLEQLETWETAGAKLLFHLRQLLKEKGLSCLVSYQDDPLTKGVDLR

301: NAQVTELLQRLHRAFVVETQPCMPQTPHRPLILKTGSKFTVTRLLVRLQEGNESLTVE

361: VSIDRNPPQLQGFRKENILTSNQKTLTPEKQSQGLIWDFGYLTVEQRSGGSGKGSNKG

421: PLGVTEELHIIISFTVKYTYQGLKQELKTDLPVVIISNMNQLSIAWASVLWFNLLSPNLQ

481: NQFFFSNPPKAPWSLLGPALSQWQESSYVGRGLNSDQLSMLRNKLFEGQNCRTEDPLLSWAD

541: FTKRESPPGKLPFWTWDKILELVHDHLKDLWNDGRIMGFVSRSQERRLLKKTMSGTFLL

601: RFSESSEGGITCSWVEHQDDDKVLIYSVQPYTKEVLSPLTEIIRHYQLLTEENIPENP

661: LRFLYPRIPRDEAFGCYYQEKVNLQERRKYLKHRLIVVSNRQVDELQQPLELKPEPELES

721: LELELGLVPEPELSLDLEPLLKAGLDLGPELESVLESTLEPVIEPTLCMVSQTVPEPDQQ

781: PVSQPVPEPLPCDLRHLNTEPMEIFRNCVKIEEIMPNGDPLLAGQNTVDEVVSRPSHF

841: YTDGPLMPSDF

FIG. 8b

113 kDa MAQWEMLQNLDSPPQDLHQLYSHSLLPVDIROYIAYWIEDQNWQEAALGSDDSKATMLF
91/84 kDa MSQWYELQQLDSKFELEQVHQLYDDS-FPMEIROXLAQWLEKQDWEHAA--NDVSFATIRF

61 FHFLDQINYEGRCSQDPESLLQHNLRKFCRDIQP-FSQDFTQLAEMIFNLLLEEKRII
57 HDLLSQIDQYSRFSLE-NNFLLQHNIRKSKRNLDQNFQEDFIQMSMIIYSCLKEERKII

120 IQAQRRAQLEQGEPVLETTPVESQHEIESRILDLRAMMEKLVKSISQLKQDQDVFCFRYK-
117 ENAQRFNQAQSGNIQSTVMLDKQKELDQKVRNVKDKVMCIEHEIKSLIEDLODEYDFKCKT

179 IQAKGKTPS--LDPHQTKQKILQETLNEEDKRRKEVLDASKAILGRITTLIE--ILLPK
177 LQNHREHETNGVAKSDQKQEQLLKKMYLMDNKRKEVVHKIIEILLNVTELTQNALINDE

235 LFEWKAAQQKACIRAPIDHGLEQIETWFTAGAKLLFHLRQLLKEKLGKLSCLVSYQDDFLT
236 LVEWKRRQQSACIGGPPNACLDQLQ-----QVRQQLKKLEELEQKYTYEHDEIT

295 KGVDLRNAQVTELLQRLHRAFVVETQPCMPQTPHRPLILKTGSKFTVTRRLLVRLQEGN
285 KNKQVLWDRFTSLFQQLIQSSFVVERQPCMPTHPORPLVLKTGVQFTVKLRLLVKKLQELN

355 ESITVEVSIQRNPPQ---LQGRKFNIILTSNQKTLTPKQGSQGLIWDFFGYITLVEQKRS
345 YNLKVKMLFDKDVNERNTVKGRKFNIILGTHTKVMNMEESTNGSLAAEFRIQLKEQKNA

412 GSGKGSNKGPLGVTEELHISFTVKYTYQGLKQELKTDTLPVVVISNMNQLSIAWASVLW
405 GT--RTNEGPLIVTEELHSISFETQLCQPLVIDLETTSLPVVVISNVSQIPSGWASILW

472 FNLLSPNLQNOFFSNPKAPWSILGPALSWQFSSYVGRGLNSDQLSMLRNKILFGQNCRT
463 YNMLVAEPRNLSFFLTPECARMAQLSEVLSWQFSSVTKRGLNVDQLNMLGEKILGPNASP

532 EDPILLSWADFTKRESPPGKLPFWTWLDKILELVHDHLKDLWNDGRIMGFVSRSQERRLLK
523 DG-LIPWTRFCKENINDKNFPFWLWIESILELIKHHLLPLWNDGCIMGFISKERERALLK

592 KTMSGTFLLRFSESS-EGGITCSWVEH-QDDDKVLIYSVQPYTKEVLOSPLLTEIIRHXYQ
582 DQQPGTFLLRFSESSREGAIFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYK

650 LLTEENIPENPLRFLYPRIIPRDEAFGCYY-----QEKVNLOERR--KYLKHLRIIVSNR
642 VMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTYIKTELISVSEV

702 QVDELQPPLELKP
702 HPSRLQTTDNLLP

FIG. 9A

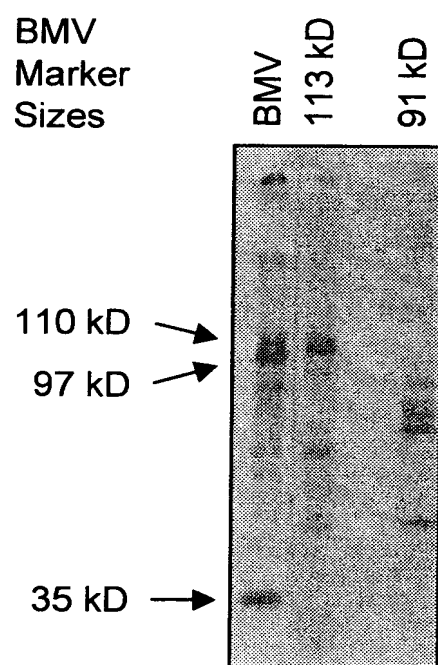


FIG. 9B

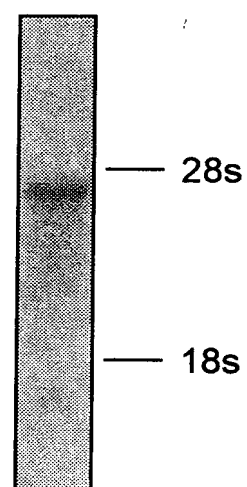


FIG. 10A

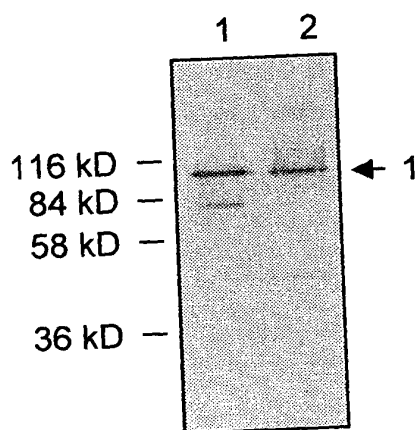


FIG. 10B

113 kD anti-serum	-	-	0.1	1	1	(μ l)
Pre-immune	-	1	-	-	+	
ISRE competition	-	-	-	-	+	
	+	+	+	+	+	

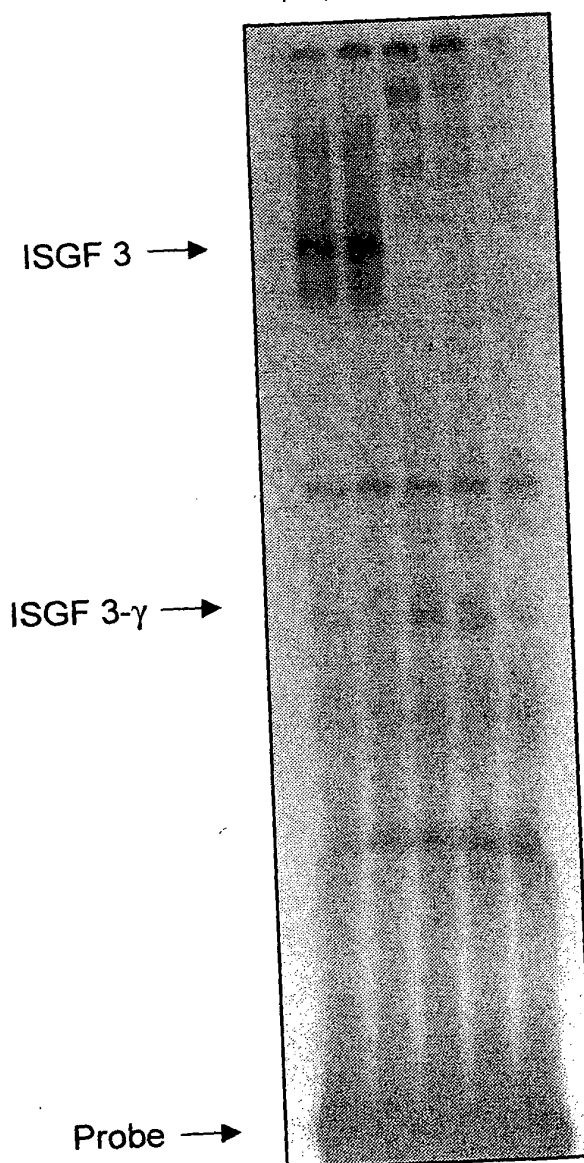


FIG. 11

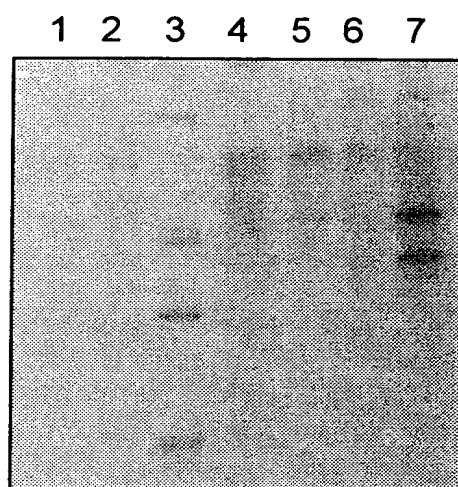


FIG. 12

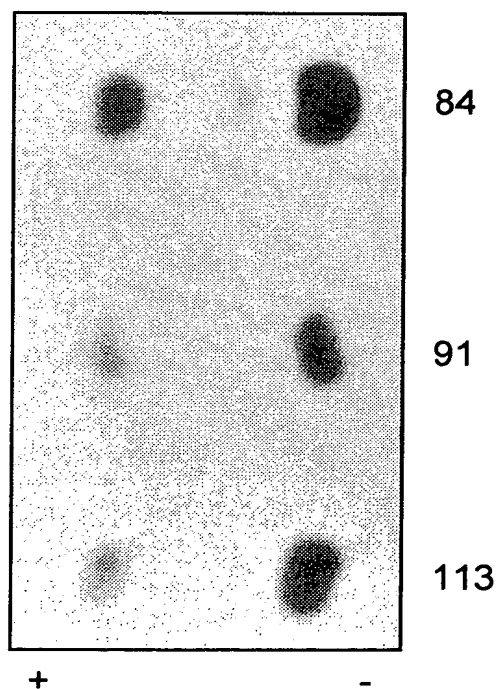


FIG. 13A

Mouse 91kD (protein)

Amino acid sequence (deduced)

1 MSQWFELQQL DSKFLEQVHQ LYDDSEFMEI RQYLAQWLEK QDWEHAAYDV
51 SFATIRFHD LLSQLDDQYSR FSLENNFLLQ HNIRKSKRNL QDNFQEDPVQ
101 MSMIIYNCLK EERKILENAQ RFNQAQEGNI QNTVMLDKQK ELDSKVRNVK
151 DQVMCIEQEI KTLLEELQDEY DFKCKTSQNR EGEANGVAKS DQKQEQLLLH
201 KMFLMLDNKR KEIIHKIREL LNSIELTQNT LINDELVEWK RRQQSACIGG
251 PPNACLDQLQ TWFTIVAETL QQIRQQLKKL EELEQKFYIE PDPITKNKQV
301 LSDRTFLLFQ QLIQSSFVVE RQPCMPHPQ RPLVLKTGVQ FTVKSRLLVK
351 LQESNLLTKV KCHFDDKDVNE KNTVKGFRKE NILGTHTKVM NMEESTNGSL
401 AAELRHLQLK EQKNAGNRTN EGPLIVTEEL HSLSFETQLC QPGLVIDLET
451 TSLPVVVISN VSQLPSGWAS ILWYNMLVTE PRNLSFFLNP PCAWWSQLSE
501 VLSWQFSSVT KRGLNADQLS MLGEKLLGPN AGPDGLIPWT RFCKENINDK
551 NFSFWPWIDT ILELIKNDLL CLWNDGCIMG FISKEERERL LKDQQPGTFL
601 LRFSESSREG AITFTWVERS QNGGEPDFIA VEPYTKKELS AVTFPDIIRN
651 YKVMAAENIP ENPLKYLYPN IDKDHAFGKY YSRPKEAPEP MELDDPKRTG
701 YIKTELISVS EVHPSRLQTT DNLLPMSPEE FDEMSRIVGP EFDSMMSTV

FIG. 13B

Mouse 91kD (protein) DNA sequence

```
1  caggatgtca cagtggttcg agcttcagca gctggactcc aagttcctgg
51  agcaggtcca ccagctgtac gatgacagtt tcccatgga aatcagacag
101  tacctggccc agtggctgga aaagcaagac tgggagcacg ctgcctatga
151  tgtctcgttt gcgaccatcc gcttccatga cctcctctca cagctggacg
201  accagtacag ccgcttttct ctggagaata atttcttggt gcagcacaac
251  atacggaaaa gcaagcgtaa tctccaggat aacttccaag aagatcccgt
301  acagatgtcc atgatcatct acaactgtct gaaggaagaa aggaagattt
351  tggaaaatgc ccaaagattt aatcaggccc aggagggaaa tattcagaac
401  actgtgatgt tagataaaca gaaggagctg gacagtaaag tcagaaatgt
451  gaaggatcaa gtcattgtgca tagagcagga aatcaagacc ctagaagaat
501  tacaagatga atatgacttt aaatgcaaaa cctctcagaa cagagaaggt
551  gaagccaatg gtgtggcgaa gagcgacca aaacaggaac agctgctgct
601  ccacaagatg tttttaatgc ttgacaataa gagaaaggag ataattcaca
```


FIG. 13C

651 aaatcagaga gttgctgaat tccatcgagc tcaactcagaa cactctgatt
701 aatgacgagc tcgtggagtg gaagcgaagg cagcagagcg cctgcatcgg
751 gggaccgccc aacgcctgcc tggatcagct gcaaacgtgg ttcaccattg
801 ttgcagagac cctgcagcag atccgtcagc agcttaaaaa gctggaggag
851 ttggaacaga aattcaccta tgagcccgac cctattacaa aaaacaagca
901 ggtgttgtca gatcgaacct tcctcctctt ccagcagctc attcagagct
951 ccttcgtggt agaacgacag ccgtgcatgc ccactcaccc gcagaggccc
1001 ctggtcttga agactggggg acagttcact gtcaagtcga gactgttggt
1051 gaaattgcaa gagtcgaatc tattaacgaa agtgaaatgt cactttgaca
1101 aagatgtgaa cgagaaaaac acagttaaag gatttcggaa gttcaacatc
1151 ttgggtacgc acacaaaagt gatgaacatg gaagaatcca ccaacggaag
1201 tctggcagct gagctccgac acctgcaact gaaggaacag aaaaacgctg
1251 ggaacagaac taatgagggg cctctcattg tcaccgaaga acttcactct
1301 cttagctttg aaaccagtt gtgccagcca ggcttggtga ttgacctgga
1351 gaccacctct cttcctgtcg tggatgctc caacgtcagc cagctcccca

FIG. 13D

1401 gtggctgggc gtctatcctg tggtaacaac tgctggtgac agagcccagg
1451 aatctctcct tcttcctgaa cccccctgac gcgtggtggt cccagctctc
1501 agaggtggtg agttggcagt tttcatcagt caccaagaga ggtctgaacg
1551 cagaccagct gagcatgctg ggagagaagc tgctggggccc taatgctggc
1601 cctgatggtc ttattccatg gacaagggtt tgtaaggaaa atattaatga
1651 taaaaatttc tccttctggc cttggattga caccatccta gagctcatta
1701 agaacgacct gctgtgcctc tggaatgatg ggtgcattat gggcttcac
1751 agcaaggagc gagaacgcgc totgctcaag gaccagcagc cagggacgtt
1801 cctgcttaga ttcagtgaga gctcccggga aggggccatc acattcacat
1851 gggtggaacg gtcccagaac ggaggtgaac ctgacttcca tgccgtggag
1901 ccctacacga aaaaagaact ttcagctggt actttcccag atattattcg
1951 caactacaaa gtcattggctg ccgagaacat accagagaat cccctgaagt
2001 atctgtacce caatattgac aaagaccacg cctttgggaa gtattattcc
2051 agaccaaagg aagcaccaga accgatggag cttgacgacc ctaagcgaac
2101 tggatacatc aagactgagt tgatttctgt gtctgaagtc cacccttcta
2151 gacttcagac cacagacaac ctgcttccca tgtctccaga ggagtttgat
2201 gagatgtccc ggatagtggg ccccgaaatt gacagtatga tgagcacagt
2251 ataaacacga atttctctct ggcgaca

FIG. 14A

13sf1 (protein)

Amino acid sequence of 13sf1

1 MSQWNQVQQL EIKFLEQVDQ FYDDNFPMEI RHLLAQWIET QDWEVASNNE
51 TMTATILLQNL LIQLDEQLGR VSKEKNLLLI HNLKRIRKVL QGKFHGNPMII
101 VAVVISNCLR EERRILAAAN MPIQGPLEKS LQSSSVSERQ RNVEHKVSAI
151 KNSVQMT EQD TKYLEDLQDE FDYRYKTIQT MDQGDKNSIL VNQEVLTL LQ
201 EMLNSLDFKR KEALSKMTQI VNETDLLMNS MLEELQDWK KRIIRIACIGG
251 PLHNGLDQLQ NCFLLAESL FQLRQOLEKL QEQSTKMTYE GDPIPAQRAH
301 LLERATEFLIY NLFKNSEFVE RHACMPTHPQ RPMVLKTLIQ FTVKLRLLIK
351 LPELNYQVKV KASIDKNVST LSNRRFVLCG THVKAMSSEE SSNGSLSVEL
401 DIATQGDEVQ YWSKGNEGCH MVTEELHSIT FETQICLYGL TINLETSSLP
451 VVMISNVSQL PNAWASIIWY NVSTNDSQNL VFFNNPPSVT LGQLLEVMSW
501 QFSSYVGRGL NSEQLNMLAE KLTVQSNYND GHILTWARECK EHILPGKTFTF
551 WTWLEAILDL IKKHILPLWI DGYIMGFVSK EKERLLLLKDK MPGTFLLRFS
601 ESHLGGITFT WVDQSENGEV RFHSVEPYNK GRLSALAFAD ILRDYKVIMA
651 ENIPENPLKY LYPDIPKDKA FGKHYSSQPC EVSRPTERGD KGYVPSVFIP
701 ISTIRSDSTE PQSPS DLLPM SPSAYAVLRE NLSPTTIETA MNSPYSAE

FIG. 14B

13sf1 (DNA)

DNA sequence of 13sf1

```
1  tgccactacc tggacggaga gagagagagc agcatgtctc agtggaatca
51  agtccaacaa ttagaaatca agtttttggg gcaagtagat cagttctatg
101 atgacaactt tcctatggaa atccggcacc tgctagctca gtggattgag
151 actcaagact ggggaagtagc ttctaacaat gaaactatgg caacaattct
201 gcttcaaaac ttactaatac aattggatga acagttgggg cgggtttcca
251 aagaaaaaaa tctgctattg attcacaatc taaagagaat tagaaaagtt
301 cttcagggca agtttcatgg aaatccaatg catgtagctg tggtaatttc
351 aaattgctta agggaagaga ggagaatatt ggctgcagcc aacatgccta
401 tccagggacc tctggagaaa tccttacaga gttcttcagt ttctgaaaga
451 caaaggaatg tggaacacaa agtgtctgcc attaaaaaca gtgtgcagat
501 gacagaacaa gataccaaat acttagaaga cctgcaagat gagtttgact
551 acaggtataa aacaattcag acaatggatc agggtgacaa aaacagtatc
601 ctggtgaacc aggaagtttt gacactgctg caagaaatgc ttaatagtct
651 ggacttcaag agaaaggaag cactcagtaa gatgacgcag atagtgaacg
701 agacagacct gctcatgaac agcatgcttc tagaagagct gcaggactgg
751 aaaaagcggc acaggattgc ctgcattggg ggcccgtcc acaatgggct
801 ggaccagctt cagaactgct ttaccctact ggcagagagt cttttccaac
851 tcagacagca actggagaaa ctacaggagc aatctactaa aatgacctat
```

FIG. 14C

13sf1 (DNA)

901 gaaggggatc ccatccctgc tcaaagagca cacctcctgg aaagagctac
951 cttectgac tacaaccttt tcaagaactc atttgtgggc gagcgacacg
1001 catgcatgcc aacgcacct cagaggccga tggacttaa aacctcatt
1051 cagttcactg taaaactgag attactaata aaattgccgg aactaaacta
1101 tcaggtgaaa gttaaaggcgt ccattgacaa gaatgtttca actctaagca
1151 atagaagatt tgtgctttgt ggaactcacg tcaaagctat gtccagtga
1201 gaatcttcca atgggagcct ctcagtgag ttagacattg caaccaagg
1251 agatgaagtg cagtactgga gttaaaggaaa cgagggtgc cacatggtga
1301 cagaggagtt gcattccata acctttgaga cccagatctg cctctatggc
1351 ctcaccatta acctagagac cagctcatta cctgtcgtga tgatttctaa
1401 tgtcagccaa ctacctaatg catgggcac catcatttgg tacaatgtat
1451 caactaacga ctcccagaac ttggttttct ttaataacct tccatctgtc
1501 actttgggcc aactcctgga agtgatgagc tggcaatttt catcctatgt
1551 cggtcgtggc cttaattcag agcagctcaa catgctggca gagaagctca
1601 cagttcagtc taactacaat gatggtcacc tcacctgggc caagttctgc
1651 aaggaacatt tgcttgga aacatttacc ttctggactt ggcttgaagc
1701 aatattggac ctaattaaaa aacatattct tccctctgg attgatgggt
1751 acatcatggg atttgttagt aaagagaagg aacggcttct gctcaaagat
1801 aaaatgcctg ggacattttt gttaagattc agtgagagcc atcttggagg

FIG. 14D

13sf1 (DNA)

1851 gataaccttc acctgggtgg accaatctga aaatggagaa gtgagattcc
1901 actctgtaga accctacaac aaagggagac tgtcggctct gcccttcgct
1951 gacatcctgc gagactacaa ggttatcatg gctgaaaaca tccctgaaaa
2001 ccctctgaag tacctctacc ctgacattcc caagacaaa gcctttggca
2051 aacactacag ctcccagccg tgcgaagtct caagaccaac cgaacgggga
2101 gacaaggggtt acgtcccctc tgttttttatc cccatttcaa caatccgaag
2151 cgattccacg gagccacaat ctcttccaga ccttctcccc atgtctccaa
2201 gtgcatatgc tgtgctgaga gaaaacctga gcccaacgac aattgaaact
2251 gcaatgaatt ccccatattc tgctgaatga cggtgcaaac ggacacttta
2301 aagaaggaag cagatgaaac tggagagtgt tctttaccat agatcacaat
2351 ttattttcttc ggctttgtaa atacc

FIG. 15A

19sf6 (DNA)

Amino acid sequence of 19sf6

1 MAQWNQLQQL DTRYLKQLHQ LYSDFPMEL RQFLAPWIES QDWAYAASKE
51 SHATLVFHNH LGEIDQQYSR FLQESNVLYQ HNLRRIKQFL QSRYLEKPME
101 IARIVARCLW EESRLLQTAA TAAQQGGQAN HPTAAVVTEK QQMLEQHLQD
151 VRKRVQDLEQ KMKVVENLQD DEDFNKYTLK SQGDMQDLNG NNQSVTRQKM
201 QQLEQMLTAL DQMRRSIVSE LAGLLSAMEY VQKTLTDEEL ADWKRRPEIA
251 CIGGPPNICL DRLENWITSL AESQLQTRQQ IKKLEELQOK VSYKGDPIVQ
301 HRPMLLEERIV ELFRNLMKSA FVVERQPCMP MHPDRPLVIK TGVQFTTKVR
351 LLVKFPELNY QLKIKVCIDK DSGDVAALRG SRKFENILGTN TKVMNMEESEN
401 NGSLSAEFKH LTLREQRCGN GGRANCDASL IVTEELHLIT FETEVYHQGL
451 KIDLETHSLP VVVISNICQM PNAWASILWY NMLTNNPKNV NEFTKPPIGT
501 WDQVAEVLWS QFSSTTKRGL SIEQLTTLAE KLLGPGVNYS GCQITWAKFC
551 KENMAGKGFS FWVWLDNIID LVKKYILALW NEGYIMGFIS KERERAILST
601 KPPGTFLRF SESSKEGGVT FTWVEKDISG KTQIQSVEPY TKQQLNNMSF
651 AEIIMGYKIM DATNILVSPL VYLYPDIPKE EAFGKYCRPE SQEIPEADPG
701 SAAPYLKTKF ICVTPTTCSN TIDLPMSPRT LDSLMQFGNN GEGAEP SAGG
751 QFESLTFDMD LTSECATSPM

FIG. 15B

19sf6 (DNA)

Amino acid sequence of 19sf6

1 gccgcgacca gccaggccgg ccagtcgggc tcagcccga gacagtcgag
51 acccctgact gcagcaggat ggctcagtgg aaccagctgc agcagctgga
101 cacacgctac ctgaagcagc tgcaccagct gtacagcgac acgttcccca
151 tggagctgcg gcagttcctg gcaccltggg ttgagagtca agactgggca
201 tatgcagcca gcaaagagtc acatgccacg ttgggtgttc ataattcttt
251 ggggtgaaatt gaccagcaat atagccgatt cctgcaagag tccaatgtcc
301 tctatcagca caaccttcga agaatacagc agtttctgca gagcaggtat
351 cttgagaagc caatggaaat tgcccggatc gtggcccgat gcctgtggga
401 agagtctcgc ctctccaga cggcagccac ggcagcccag caagggggcc
451 aggccaaacca cccaacagcc gccgtagtga cagagaagca gcagatgttg
501 gagcagcatc ttcaggatgt ccggaagcga gtgcaggatc tagaacagaa
551 aatgaaggtg gtggagaacc tccaggacga ctttgatttc aactacaaaa
601 ccctcaagag ccaaggagac atgcaggatc tgaatggaaa caaccagtct
651 gtgaccagac agaagatgca gcagctggaa cagatgctca cagccctgga
701 ccagatgcgg agaagcattg tgagtgaact ggcggggctc ttgtcagcaa
751 tggagtacgt gcagaagaca ctgactgatg aagagctggc tgactggaag
801 aggcggccag agatcgctg catcggaggc cctcccaaca tctgcctgga
851 ccgtctggaa aactggataa cttcattagc agaattctca cttcagaccc

FIG. 15C

19sf6 (DNA)

901 gccacaacaaat taagaaactg gaggagctgc agcagaaaagt gtccatacaag
951 ggcgacccta tcgtgcagca ccggcccatg ctggaggaga ggatcgtgga
1001 gctgttcaga aacttaatga agagtgcctt cgtggtggag cggcagccct
1051 gcatgcccat gcacccggac cggcccttag tcatcaagac tgggtgccag
1101 tttaccacga aagtcagggtt gctggtcaaa tttcctgagt tgaattatca
1151 gcttaaaatt aaagtgtgca ttgataaaga ctctggggat gttgctgccc
1201 tcagaggggtc tcggaaattt aacattctgg gcacgaacac aaaagtgatg
1251 aacatggagg agtctaacaa cggcagcctg tctgcagagt tcaagcacct
1301 gacccttagg gagcagagat gtgggaatgg aggccgtgcc aattgtgatg
1351 cctccttgat cgtgactgag gagctgcacc tgatcacctt cgagactgag
1401 gtgtaccacc aaggcctcaa gattgaccta gagaccact ccttgccagt
1451 tgtggtgatc tccaacatct gtcagatgcc aaatgcttgg gcatcaatcc
1501 tgtggtataa catgctgacc aataacccca agaacgtgaa cttcttcaact
1551 aagccgccaa ttggaacctg ggaccaagtg gccgaggtgc tcagctggca
1601 gttctcgtcc accaccaagc gagggctgag catcgagcag ctgacaacgc
1651 tggctgagaa gtccttaggg cctggtgtga actactcagg gtgtcagatc
1701 acatgggcta aattctgcaa agaaaacatg gctggcaagg gcttctcctt
1751 ctgggtctgg ctagacaata tcatcgacct tgtgaaaaag tatactcttg
1801 ccctttggaa tgaagggtac atcatgggtt tcatcagcaa ggagcgggag

FIG. 15D

19sf6 (DNA)

1851 cgggccatcc taagcacaaa gcccccgggc accttcctac tgcgcttcag
1901 cgagagcagc aaagaaggag gggtcacttt cacttgggtg gaaaaggaca
1951 tcagtggcaa gaccagatc cagtctgtag agccatacac caagcagcag
2001 ctgaacaaca tgtcatttgc tgaaatcadc atgggctata agatcatgga
2051 tgcgaccaac atcctggtgt ctccacttgt ctacctctac cccgacattc
2101 ccaaggagga ggcatttgga aagtactgta ggcccagagag ccaggagcac
2151 cccgaagccg acccaggtag tgctgccccg tacctgaaga ccaagttcat
2201 ctgtgtgaca ccaacgacct gcagcaatac cattgacctg ccgatgtccc
2251 cccgcacttt agattcattg atgcagtttg gaaataacgg tgaagggtgct
2301 gagccctcag caggagggca gtttgagtcg ctcacgtttg acatggatct
2351 gacctcggag tgtgctacct ccccatgtg aggagctgaa accagaagct
2401 gcagagacgt gacttgagac acctgccccg tgctccacce ctaagcagcc
2451 gaaccccata tcgtctgaaa ctctaactt tgtggttcca gatttttttt
2501 tttaatttcc tacttctgct atctttgggc aatctgggca ctttttaaaa
2551 gagagaaatg agtgagtgtg ggtgataaac tgbtatgtaa agaggagaga
2601 cctctgagtc tggggatggg gctgagagca gaagggaggc aaaggggaac
2651 acctcctgtc ctgcccgcct gccctccttt ttcagcagct cggggggttg
2701 ttgttagaca agtgccctct ggtgcccatt gctacctgtt gccccactct
2751 gtgagctgat accccattct ggggaactct ggctctgcac tttcaacctt

FIG. 15E

19sf6 (DNA)

2001 gctaatatcc acatagaagc taggactaag cccaggaggt tcctctttaa

2051 attaaaaaaaa aaaaaaaaaa

FIG. 16A

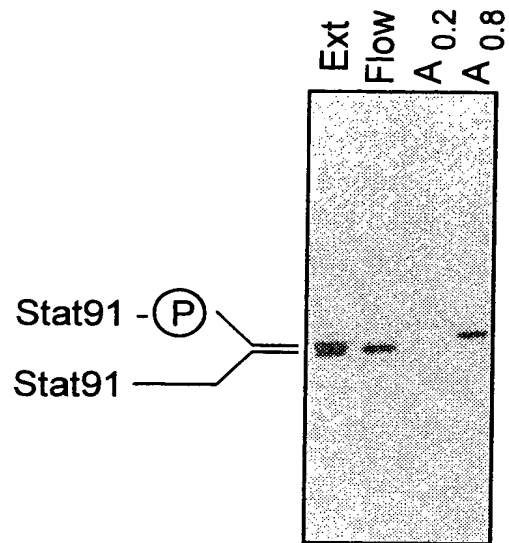


FIG. 16B

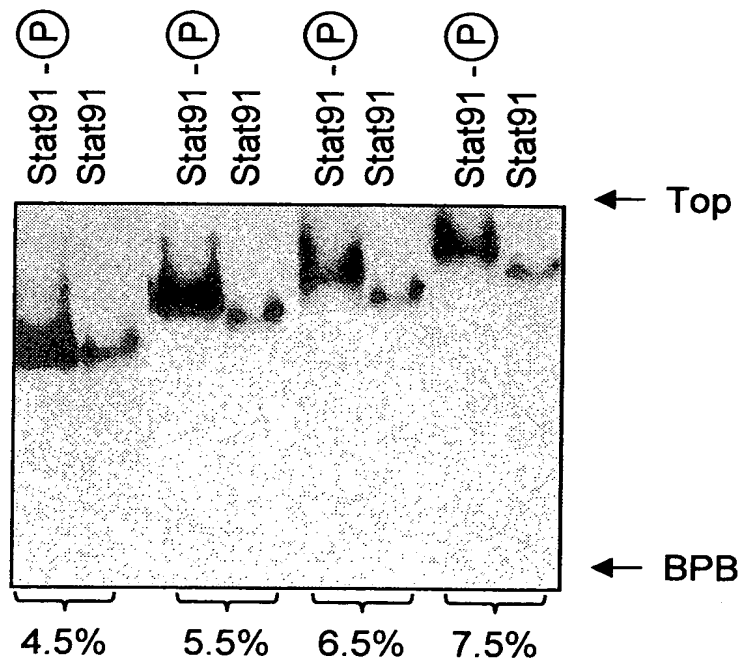


FIG.16C

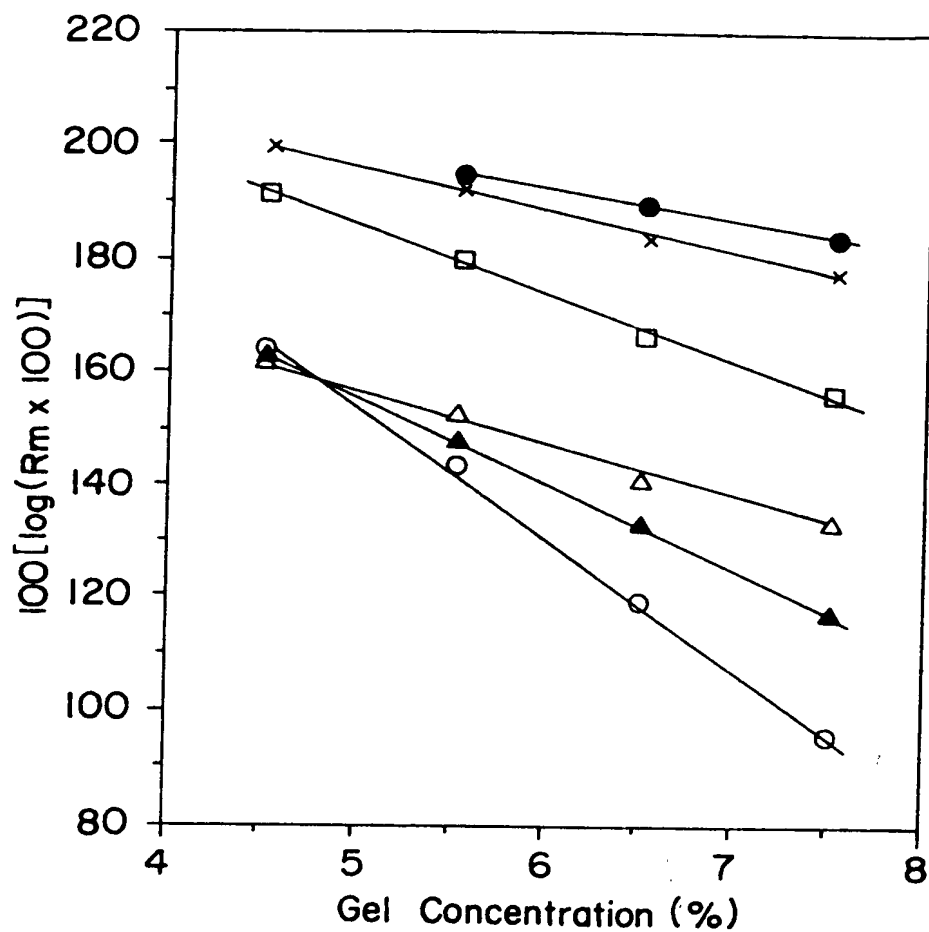


FIG.16D

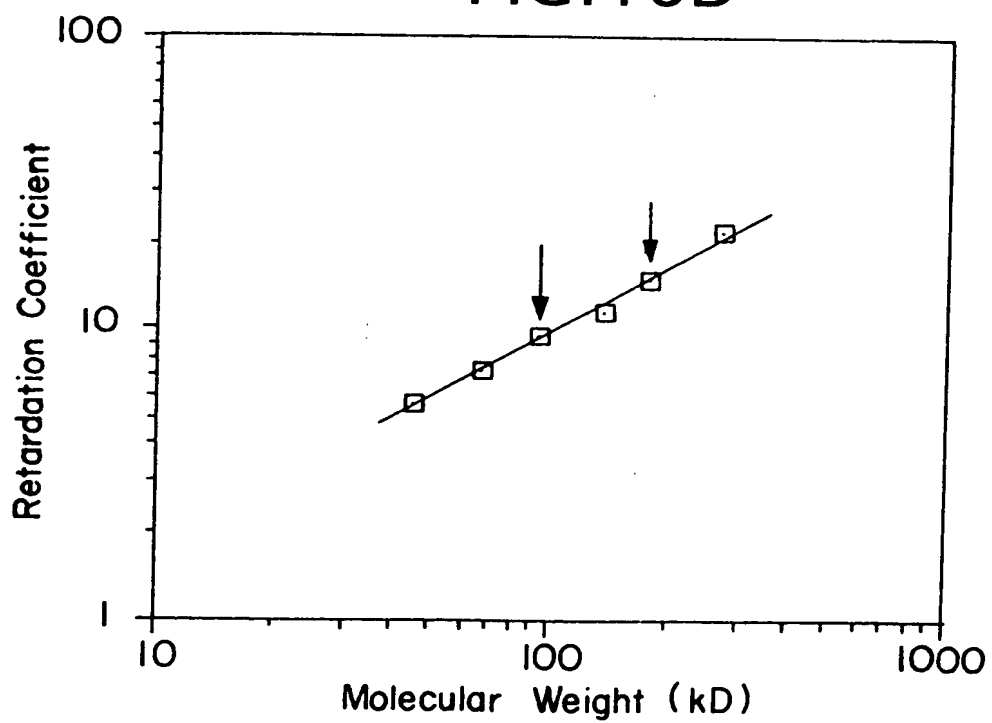


FIG. 17A

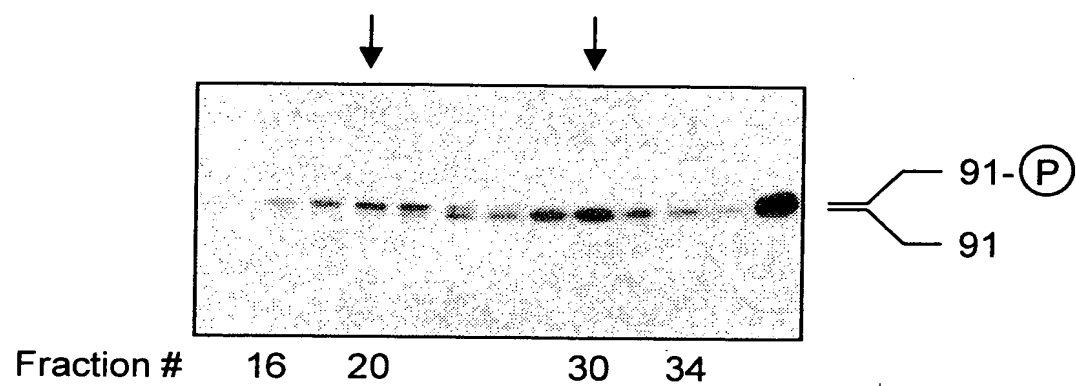


FIG. 17B

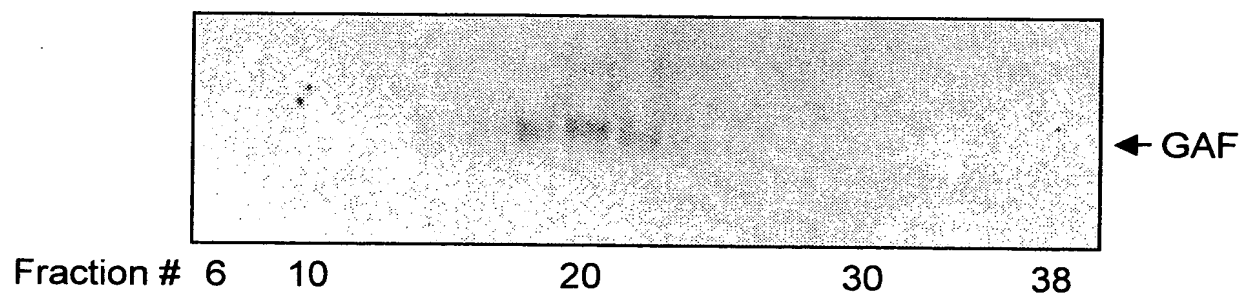


FIG.17C

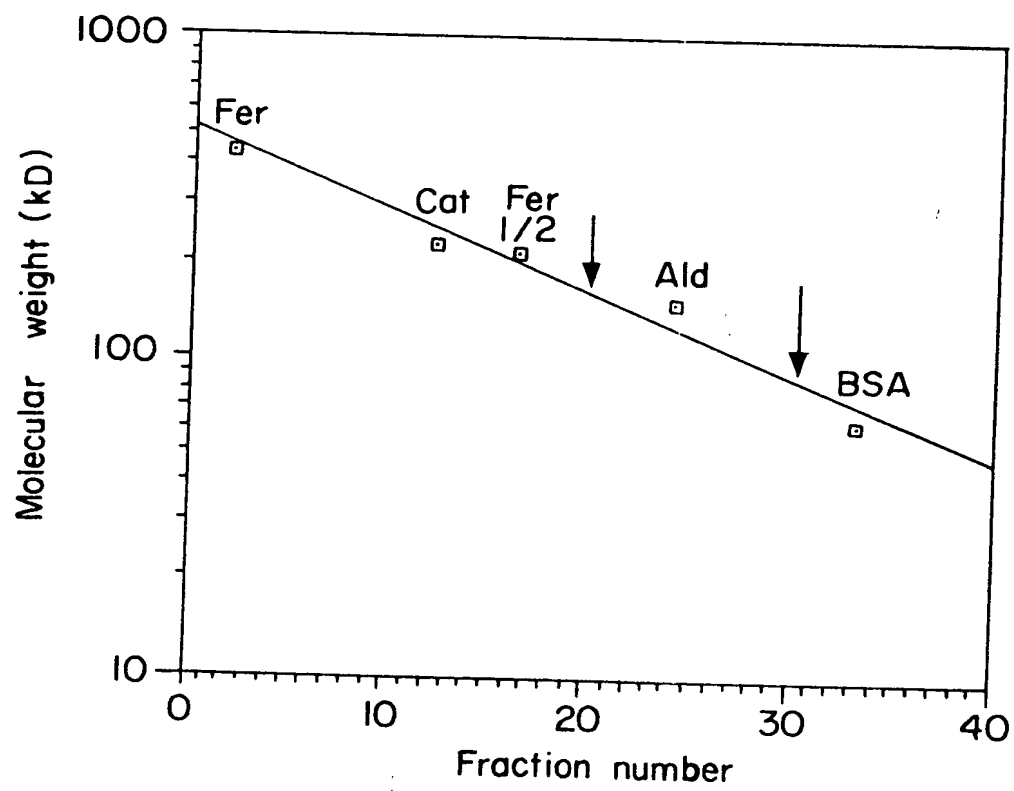


FIG. 18A

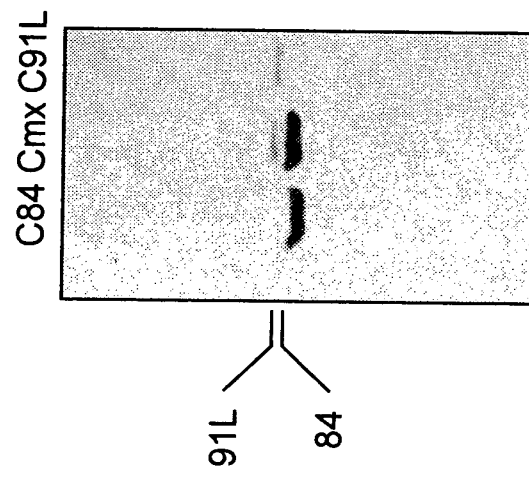


FIG. 18B

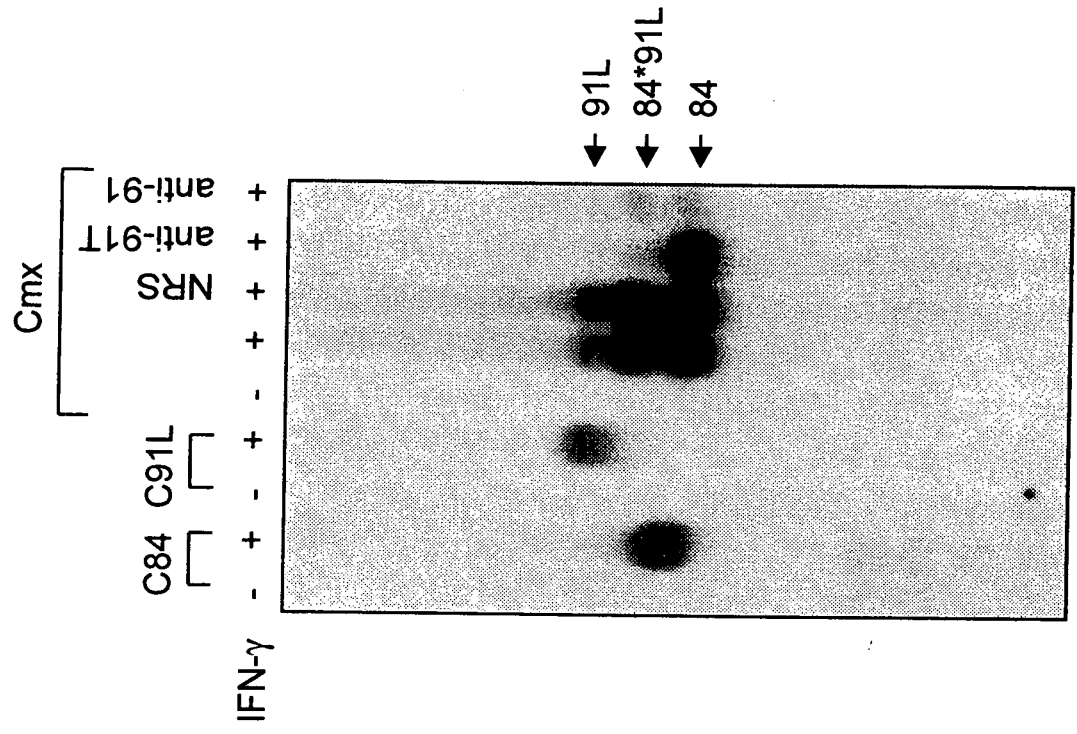


FIG. 19

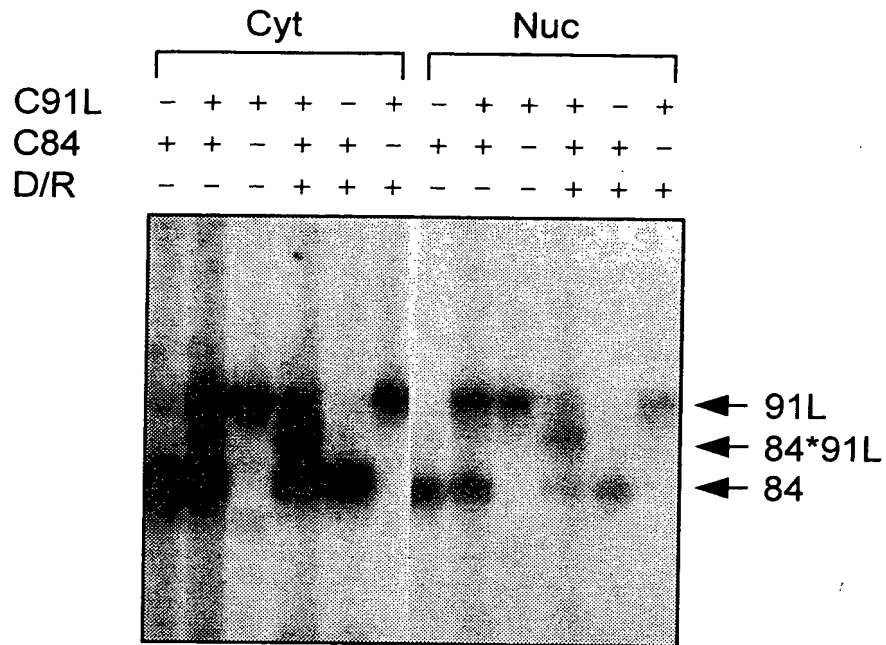


FIG. 20

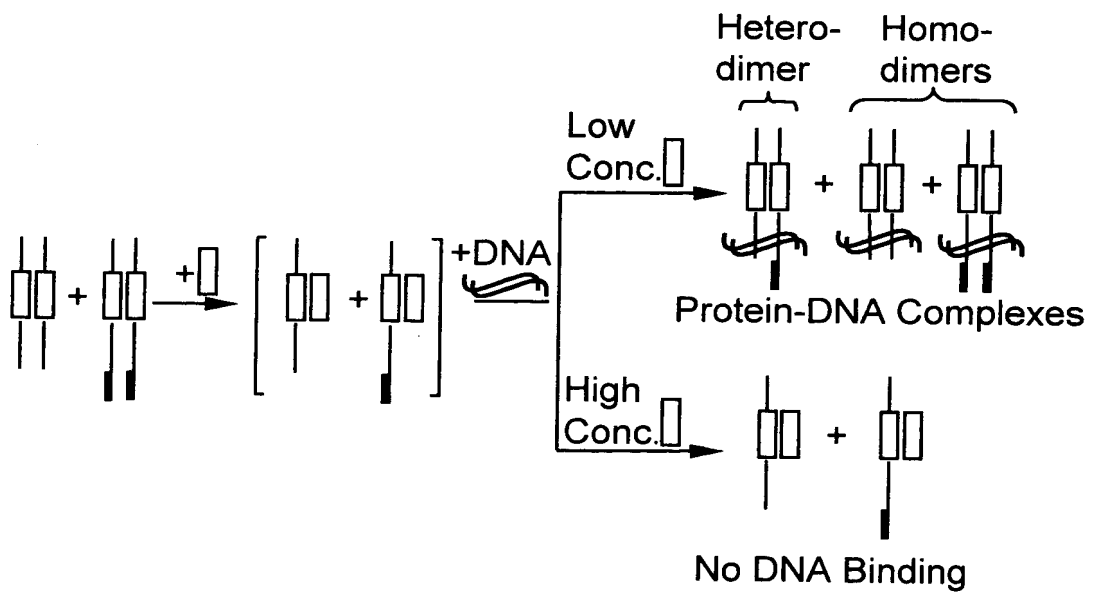


FIG. 21

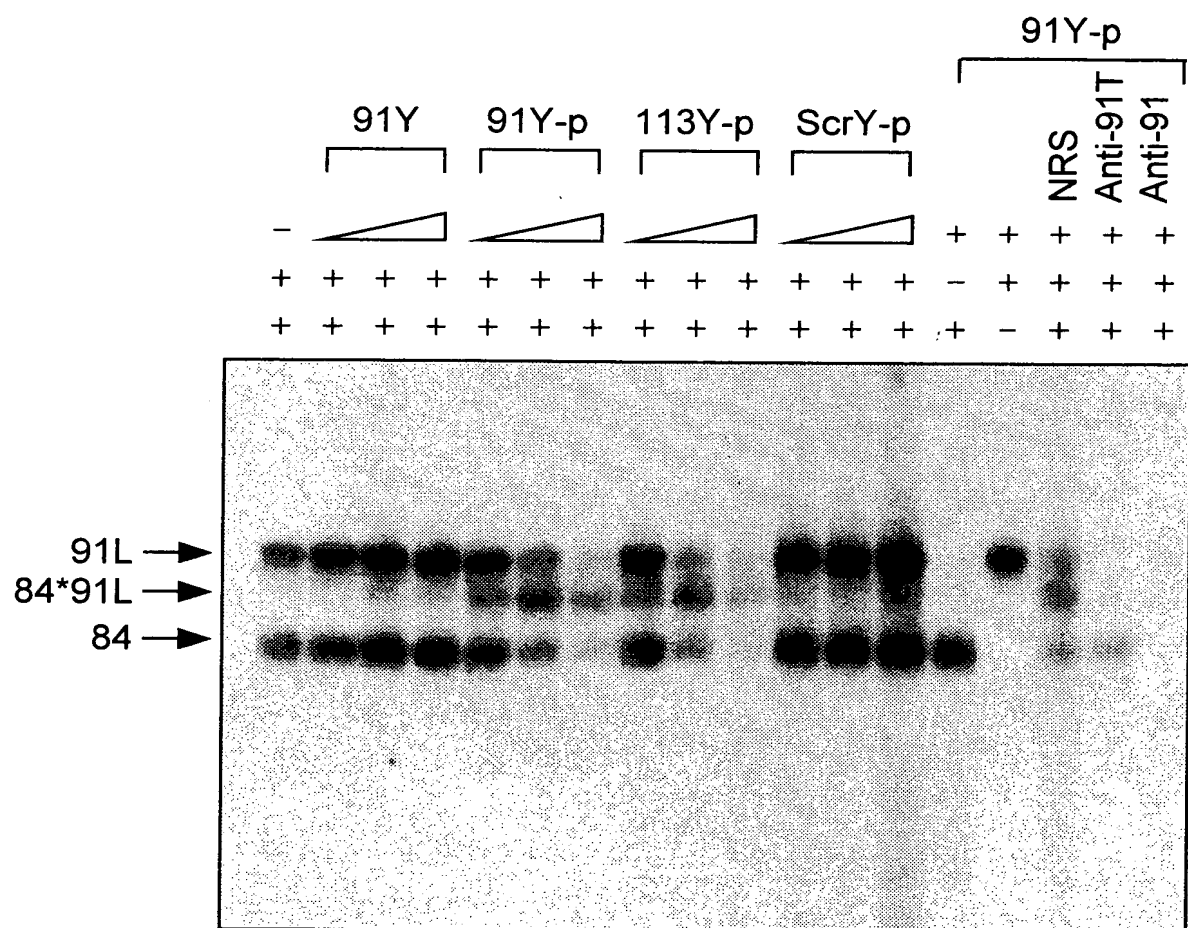


FIG. 22A

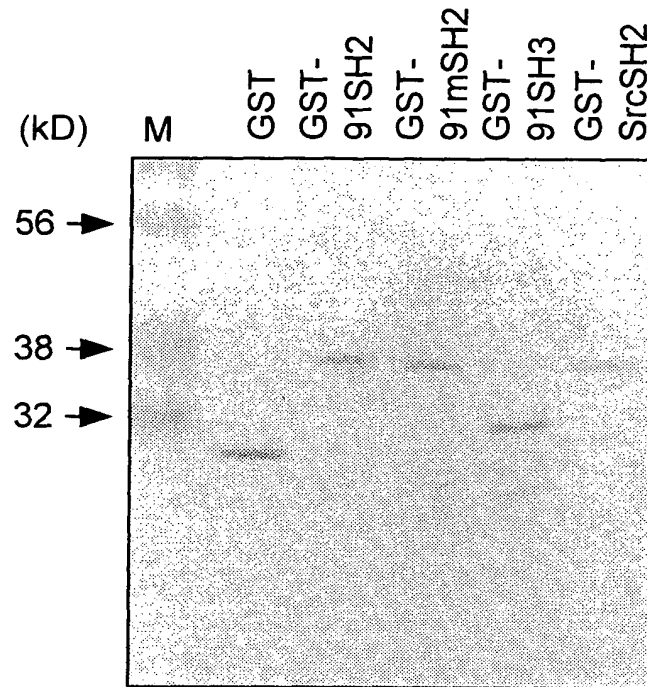


FIG. 22B

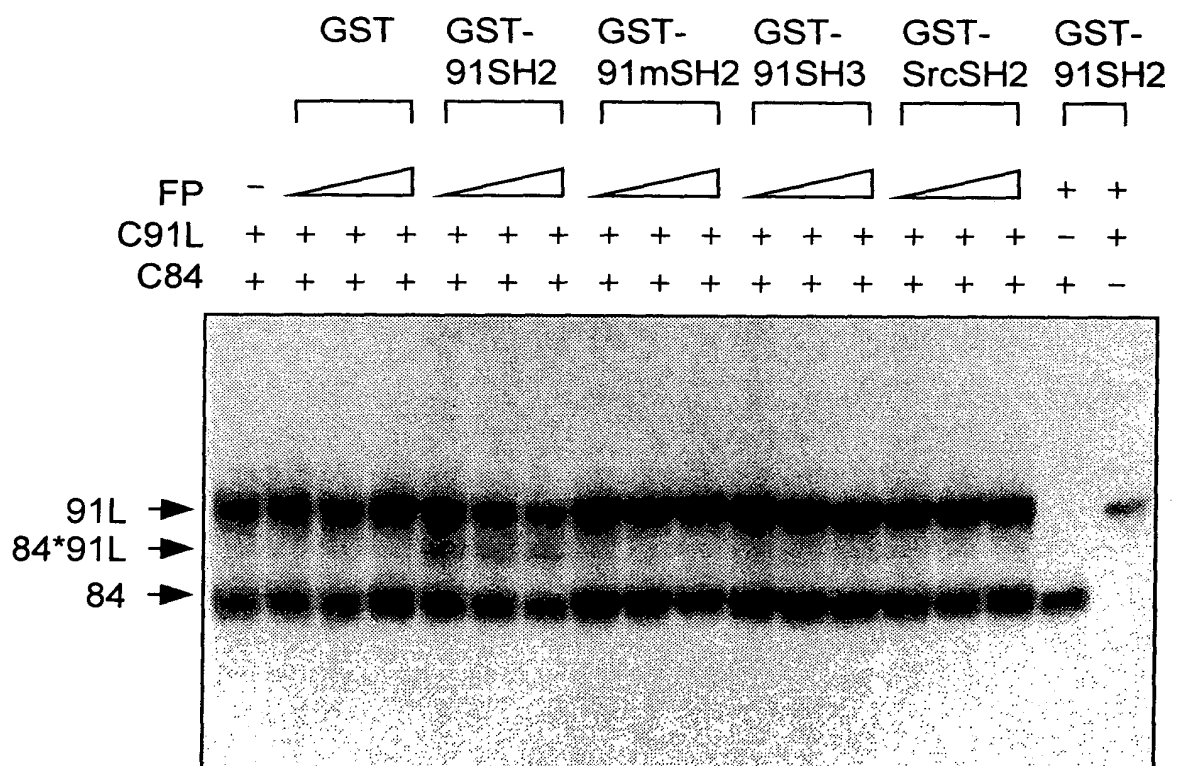


FIG.23A

	$\beta A1$	$\alpha A2$	$\beta B5$	
stat91 (569)	LLPL WND GRCIMGFI SKERERALLK DQOP	G TFLLRFS	ESSRE	G AITFWVER (619)
src (145)	AEE WYF GXI	TRRESERLLL NPENPRG	TFLVRES	ETTK G AYCLSVSD (188)
lck (127)	WFF XNL	SRKDAEROLL APGNTHG	SFLIRES	ESTA G SFSLSVRD (168)
abl (141)	EKHS WYH GPV	SRNAAEYLLS SGIN	G SFLVRES	DRRP G QRSISLRY (184)
p85 α N (330)	QDAE WYW GDI	SREEVNEKLR DTAD	G TFLVRDA	STQMH G DYTTLTRK (374)

SCR'S	XXX	XXXXXXXXXX	XXXXX	XXX	XXXXXX
	[--] [-]	[-----] [-----]	[-----] [-----]	[-----] [-----]	[-----] [-----]
Name	NA	βA	AA	αA	AB
					βB
					BC
					βC

	$\beta D6$	
stat91 (620)	S Q N	GGEPDFHAVEPYTKKELSAVTFP IIRNYKV MAA ENIPENPL (664)
	D	
src (189)	F FD NAK GL	NVGHYKI RKL DS G (210)
lck (169)	D FD QNQ GE	VVGHYKI RNL DN G (189)
abl (185)	E E G	RVGHYRI NTA SD G (200)
p85 α N (375)	GG	NNKLIKI FHR D G (388)

SCR'S	XXXXXXXX X	X
	[-----] [-----]	[-----] [-----]
Name	CD	βD $\beta D'$ DE

FIG.23B

stat91	(665)	KYLY	P	NID	K	KDHAFGKYYSRP	PK	EA	PEP	M	ELD	GP	KG	GT	GY	IKT	(704)
src	(211)	GFYI	TSR	TQF	S	SLQQLVAYYSKH	AD	GL	CH		RLT	NVC	PTS				(248)
lck	(190)	GFYI	SPR	ITF	P	GLHDLVRHYTNA	SD	GL	CT		RLS	RPC	QTQ				(227)
abl	(201)	KLIV	SSE	SRF	N	TLAELVHHHSTV	AD	GL	IT		TLH	YPA	PKR				(238)
p85αN	(389)	KYGF	SDP	LTF	N	SVVELINHYRHE	S	LA	QYN	PKLDV	KL	L	Y	P			(427)
αB9																	
SCR'S		XXX				XXXXXXXXXX											
Name		[--]	[--]	[--]		[-----]					[-----]						
		βE	EF	βF		αB					BG						βG GΩ